

(FILE 'HOME' ENTERED AT 10:23:53 ON 29 APR 2002)

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 10:24:21 ON 29 APR 2002

L1 892 S BRCA1 AND (PCR OR POLYMERASE (W) CHAIN)
L2 30 S L1 AND (EXON (2A) (13 OR 22))
L3 14 DUP REM L2 (16 DUPLICATES REMOVED)

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L4 ANSWER 1 OF 5 MEDLINE DUPLICATE 1
 AN 97029994 MEDLINE
 DN 97029994 PubMed ID: 8875917
 TI Clinical and pathological features of ovarian cancer in women with germ-line mutations of **BRCA1**.
 CM Comment in: N Engl J Med. 1996 Nov 7;336(19):1455-6
 Comment in: N Engl J Med. 1997 Apr 24;336(17):1254-5; discussion 1256-7
 Comment in: N Engl J Med. 1997 Apr 24;336(17):1254; discussion 1256-7
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 Comment in: N Engl J Med. 1997 Apr 24;336(17):1255; discussion 1256-7
 Comment in: N Engl J Med. 1997 Apr 24;336(17):1256; discussion 1256-7
 AU Rubin S C; Benjamin I; Behbakht K; Takahashi H; Morgan M A; LiVolsi V A; Berchuck A; Muto M G; Garber J E; Weber B L; Lynch H T; Boyd J
 CS Department of Obstetrics and Gynecology, University of Pennsylvania Medical Center, Philadelphia, PA 19104, USA.
 SO NEW ENGLAND JOURNAL OF MEDICINE, (1996 Nov 7) 335 (19) 1413-6.
 Journal code: NOW; 0255562. ISSN: 0028-4793.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Abridged Index Medicus Journals; Priority Journals
 EM 199611
 ED Entered STN: 19961219
 Last Updated on STN: 19980206
 Entered Medline: 19961114
 AB BACKGROUND: We tested the hypothesis that ovarian cancers associated with germ-line mutations of **BRCA1** have distinct clinical and pathological features as compared with sporadic ovarian cancers. METHODS: We reviewed clinical and pathological data on patients with primary epithelial ovarian cancer found to have germ-line mutations of **BRCA1**. Survival among patients with advanced-stage cancer and such mutations was compared with that in control patients matched stage, grade, and histologic subtype of the tumors. A combination of single-strand conformation and sequencing analyses was used to examine the 22 coding **exons** and intronic splice-donor and splice-acceptor regions of **BRCA1** for mutations in pathological specimens. Alternatively, some patients were known to be obligate carriers of the mutant **BRCA1** gene because of their parental relationships with documented mutant-gene carriers. RESULTS: We identified 53 patients with germ-line mutations of **BRCA1**. The average age at diagnosis was 48 years (range, 28 to 78). Histologic examination in 43 of the 53 patients showed serous adenocarcinoma. Thirty-seven tumors were of grade 3, 11 were of grade 2, 2 were of grade 1, and 3 were of low malignant potential. In 38 patients, the tumors were of stage III; 9 patients (including those with tumors of low malignant potential) had stage I disease, 5 had stage IV, and 1 had stage II. As of June 1996, with a median follow-up among survivors of 71 months from diagnosis, 20 patients had died of ovarian cancer, 27 had no evidence of the disease, 4 were alive with the disease, and 2 had died of other diseases. Actuarial median survival for the 43 patients with and advanced-stage disease was 77 months, as compared with 29 months for the matched controls ($P<0.001$). CONCLUSIONS: As compared with sporadic ovarian cancers, cancers associated with **BRCA1** mutation appear to have a significantly more favorable clinical course.

L4 ANSWER 2 OF 5 MEDLINE DUPLICATE 2
 AN 96225458 MEDLINE
 DN 96225458 PubMed ID: 8640237
 TI Mutation analysis in the **BRCA2** gene in primary breast cancers.
 AU Miki Y; Katagiri T; Kasumi F; Yoshimoto T; Nakamura Y
 CS Department of Human Genome Analysis, Cancer Chemotherapy Center, Tokyo,

Japan.

SO NATURE GENETICS, (1996 Jun) 13 (2) 245-7.
Journal code: BRO; 9216904. ISSN: 1061-4036.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

OS GENBANK-D83989

EM 199607

ED Entered STN: 19960726
Last Updated on STN: 19990129
Entered Medline: 19960716

AB Breast cancer, one of the most common and deleterious of all diseases affecting women, occurs in hereditary and sporadic forms. Hereditary breast cancers are genetically heterogeneous; susceptibility is variously attributable to germline mutations in the **BRCA1** (ref. 1), **BRCA2** (ref. 2), **TP53** (ref. 3) or ataxia telangiectasia (**ATM**) genes, each of which is considered to be a tumour suppressor. Recently a number of germline mutations in the **BRCA2** gene have been identified in families prone to breast cancer. We screened 100 primary breast cancers from Japanese patients for **BRCA2** mutations, using PCR-SSCP. We found two germline mutations and one somatic mutation in our patient group. One of the germline mutations was an insertion of an Alu element into **exon 22**, which resulted in alternative splicing that skipped **exon 22**. The presence of a 64-bp polyadenylate tract and evidence for an 8-bp target-site duplication of the inserted DNA implied that the retrotransposal insertion of a transcriptionally active Alu element caused this event. Our results indicate that somatic **BRCA2** mutations, like somatic mutations in the **BRCA1** gene, are very rare in primary breast cancers.

L4 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2002 ACS

AN 1997:146761 CAPLUS

DN 126:181894

TI A protein truncation test for **BRCA1**

AU Garvin, Alex M.; Mueller, HJ.; Scott, Rodney J.

CS Dep. Genetics, Children's Hosp., Basel, Switz.

SO Hered. Cancer, Int. Res. Conf. Fam. Cancer, 2nd (1996), Meeting Date 1995, 6-10. Editor(s): Mueller, Hansjakob; Scott, Rodney J.; Weber, Walter. Publisher: Karger, Basel, Switz.
CODEN: 64BIAV

DT Conference

LA English

AB The recently isolated **BRCA1** gene [1] spans 100 kb of chromosome 17q21 and contains 1,863 codons dispersed on **22 exons**. Screening for mutations in **BRCA1** by single-strand conformation polymorphism (SSCP) or sequencing requires as many as 50 PCR reactions followed by anal. of the 50 amplified products [2]. Such a work-intensive endeavor makes large-scale screening of **BRCA1** problematic. One way of reducing the amt. of work required to screen coding sequence is to perform a protein truncation test (PTT) [3], in which the coding sequence is PCR amplified with an RNA polymerase binding site attached to its 5' end. The PCR product is then used as template in a coupled in vitro transcription/translation reaction and the radiolabeled protein product is analyzed by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). PTT has been successful in screening for mutations in the APC tumor suppressor gene [4]. Since 86% of all mutations found in **BRCA1** result in a truncated protein product [5], **BRCA1** is an esp. attractive candidate for screening by PTT. Below the authors will describe a PTT capable of screening the entire coding region of **BRCA1** using 7 PCR per screen. The authors also show an example of a mutation in **BRCA1** detected using this assay.

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@PJL JOB NAME = "MSJOB 23"

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@PJL USTATUS PAGE = OFF

@PJL USTATUS DEVICE = ON

@PJL USTATUS TIMED = 30

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detected in any of the tumors, constitutional mutations were identified in four cases: two frameshifts, one nonsense mutation and one intronic base substitution 32 bp downstream of **exon 22**; RT-PCR experiments revealed that the single-base substitution in the intron seemed to increase the transcript lacking **exon 22**. All four cases were judged to involve truncation of the gene product. The evidence reported here supports a rather limited role of **BRCA1** in ovarian carcinogenesis in the Japanese population.

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